

## SEQUENCE LISTING

<110> Sagami Chemical Research Center,  
Protegene Inc.

<120> Human proteins having hydrophobic domains and DNAs encoding these  
proteins

<130> 661926

<150> JP 11-194359

<151> 1999-07-08

<160> 30

<210> 1

<211> 339

<212> PRT

<213> Homo sapiens

<400> 1

Met Ser Pro Ser Pro Thr Ala Leu Phe Cys Leu Gly Leu Cys Leu Gly

1

5

10

15

Arg Val Pro Ala Gln Ser Gly Pro Leu Pro Lys Pro Ser Leu Gln Ala

20

25

30

Leu Pro Ser Ser Leu Val Pro Leu Glu Lys Pro Val Thr Leu Arg Cys  
35 40 45  
Gln Gly Pro Pro Gly Val Asp Leu Tyr Arg Leu Glu Lys Leu Ser Ser  
50 55 60  
Ser Arg Tyr Gln Asp Gln Ala Val Leu Phe Ile Pro Ala Met Lys Arg  
65 70 75 80  
Ser Leu Ala Gly Arg Tyr Arg Cys Ser Tyr Gln Asn Gly Ser Leu Trp  
85 90 95  
Ser Leu Pro Ser Asp Gln Leu Glu Leu Val Ala Thr Gly Val Phe Ala  
100 105 110  
Lys Pro Ser Leu Ser Ala Gln Pro Gly Pro Ala Val Ser Ser Gly Gly  
115 120 125  
Asp Val Thr Leu Gln Cys Gln Thr Arg Tyr Gly Phe Asp Gln Phe Ala  
130 135 140  
Leu Tyr Lys Glu Gly Asp Pro Ala Pro Tyr Lys Asn Pro Glu Arg Trp  
145 150 155 160  
Tyr Arg Ala Ser Phe Pro Ile Ile Thr Val Thr Ala Ala His Ser Gly  
165 170 175  
Thr Tyr Arg Cys Tyr Ser Phe Ser Ser Arg Asp Pro Tyr Leu Trp Ser  
180 185 190  
Ala Pro Ser Asp Pro Leu Glu Leu Val Val Thr Gly Thr Ser Val Thr  
195 200 205  
Pro Ser Arg Leu Pro Thr Glu Pro Pro Ser Ser Val Ala Glu Phe Ser  
210 215 220  
Glu Ala Thr Ala Glu Leu Thr Val Ser Phe Thr Asn Glu Val Phe Thr

225                      230                      235                      240  
Thr Glu Thr Ser Arg Ser Ile Thr Ala Ser Pro Lys Glu Ser Asp Ser  
245                      250                      255  
Pro Ala Gly Pro Ala Arg Gln Tyr Tyr Thr Lys Gly Asn Leu Val Arg  
260                      265                      270  
Ile Cys Leu Gly Ala Val Ile Leu Ile Ile Leu Ala Gly Phe Leu Ala  
275                      280                      285  
Glu Asp Trp His Ser Arg Arg Lys Arg Leu Arg His Arg Gly Arg Ala  
290                      295                      300  
Val Gln Arg Pro Leu Pro Pro Leu Pro Pro Leu Pro Leu Thr Arg Lys  
305                      310                      315                      320  
Ser His Gly Gly Gln Asp Gly Gly Arg Gln Asp Val His Ser Arg Gly  
325                      330                      335  
Leu Cys Ser

&lt;210&gt; 2

&lt;211&gt; 487

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

Met Ala Ser Ser Ala Glu Gly Asp Glu Gly Thr Val Val Ala Leu Ala  
1                      5                      10                      15  
Gly Val Leu Gln Ser Gly Phe Gln Glu Leu Ser Leu Asn Lys Leu Ala

20 25 30  
Thr Ser Leu Gly Ala Ser Glu Gln Ala Leu Arg Leu Ile Ile Ser Ile  
35 40 45  
Phe Leu Gly Tyr Pro Phe Ala Leu Phe Tyr Arg His Tyr Leu Phe Tyr  
50 55 60  
Lys Glu Thr Tyr Leu Ile His Leu Phe His Thr Phe Thr Gly Leu Ser  
65 70 75 80  
Ile Ala Tyr Phe Asn Phe Gly Asn Gln Leu Tyr His Ser Leu Leu Cys  
85 90 95  
Ile Val Leu Gln Phe Leu Ile Leu Arg Leu Met Gly Arg Thr Ile Thr  
100 105 110  
Ala Val Leu Thr Thr Phe Cys Phe Gln Met Ala Tyr Leu Leu Ala Gly  
115 120 125  
Tyr Tyr Tyr Thr Ala Thr Gly Asn Tyr Asp Ile Lys Trp Thr Met Pro  
130 135 140  
His Cys Val Leu Thr Leu Lys Leu Ile Gly Leu Ala Val Asp Tyr Phe  
145 150 155 160  
Asp Gly Gly Lys Asp Gln Asn Ser Leu Ser Ser Glu Gln Gln Lys Tyr  
165 170 175  
Ala Ile Arg Gly Val Pro Ser Leu Leu Glu Val Ala Gly Phe Ser Tyr  
180 185 190  
Phe Tyr Gly Ala Phe Leu Val Gly Pro Gln Phe Ser Met Asn His Tyr  
195 200 205  
Met Lys Leu Val Gln Gly Glu Leu Ile Asp Ile Pro Gly Lys Ile Pro  
210 215 220

Asn Ser Ile Ile Pro Ala Leu Lys Arg Leu Ser Leu Gly Leu Phe Tyr  
225 230 235 240  
Leu Val Gly Tyr Thr Leu Leu Ser Pro His Ile Thr Glu Asp Tyr Leu  
245 250 255  
Leu Thr Glu Asp Tyr Asp Asn His Pro Phe Trp Phe Arg Cys Met Tyr  
260 265 270  
Met Leu Ile Trp Gly Lys Phe Val Leu Tyr Lys Tyr Val Thr Cys Trp  
275 280 285  
Leu Val Thr Glu Gly Val Cys Ile Leu Thr Gly Leu Gly Phe Asn Gly  
290 295 300  
Phe Glu Glu Lys Gly Lys Ala Lys Trp Asp Ala Cys Ala Asn Met Lys  
305 310 315 320  
Val Trp Leu Phe Glu Thr Asn Pro Arg Phe Thr Gly Thr Ile Ala Ser  
325 330 335  
Phe Asn Ile Asn Thr Asn Ala Trp Val Ala Arg Tyr Ile Phe Lys Arg  
340 345 350  
Leu Lys Phe Leu Gly Asn Lys Glu Leu Ser Gln Gly Leu Ser Leu Leu  
355 360 365  
Phe Leu Ala Leu Trp His Gly Leu His Ser Gly Tyr Leu Val Cys Phe  
370 375 380  
Gln Met Glu Phe Leu Ile Val Ile Val Glu Arg Gln Ala Ala Arg Leu  
385 390 395 400  
Ile Gln Glu Ser Pro Thr Leu Ser Lys Leu Ala Ala Ile Thr Val Leu  
405 410 415  
Gln Pro Phe Tyr Tyr Leu Val Gln Gln Thr Ile His Trp Leu Phe Met

420 425 430  
Gly Tyr Ser Met Thr Ala Phe Cys Leu Phe Thr Trp Asp Lys Trp Leu  
435 440 445  
Lys Val Tyr Lys Ser Ile Tyr Phe Leu Gly His Ile Phe Phe Leu Ser  
450 455 460  
Leu Leu Phe Ile Leu Pro Tyr Ile His Lys Ala Met Val Pro Arg Lys  
465 470 475 480  
Glu Lys Leu Lys Lys Met Glu  
485

&lt;210&gt; 3

&lt;211&gt; 262

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

Met Ala Ala Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu Leu  
1 5 10 15  
Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys Arg Ala  
20 25 30  
Gly Thr Gly Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu Gly Glu Ala  
35 40 45  
Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe Glu Ile Asp Asp  
50 55 60  
Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu Trp Asn Gln Gln Asp

260

&lt;210&gt; 4

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

Met Gln Pro Pro Val Pro Gly Pro Leu Gly Leu Leu Asp Pro Ala Glu  
1 5 10 15  
Gly Leu Ser Arg Arg Lys Lys Thr Ser Leu Trp Phe Val Gly Ser Leu  
20 25 30  
Leu Leu Val Ser Val Leu Ile Val Thr Val Gly Leu Ala Ala Thr Thr  
35 40 45  
Arg Thr Glu Asn Val Thr Val Gly Gly Tyr Tyr Pro Gly Ile Ile Leu  
50 55 60  
Gly Phe Gly Ser Phe Leu Gly Ile Ile Gly Ile Asn Leu Val Glu Asn  
65 70 75 80  
Arg Arg Gln Met Leu Val Ala Ala Ile Val Phe Ile Ser Phe Gly Val  
85 90 95  
Val Ala Ala Phe Cys Cys Ala Ile Val Asp Gly Val Phe Ala Ala Gln  
100 105 110  
His Ile Glu Pro Arg Pro Leu Thr Thr Gly Arg Cys Gln Phe Tyr Ser  
115 120 125  
Ser Gly Val Gly Tyr Leu Tyr Asp Val Tyr Gln Thr Glu Val Ser Arg  
130 135 140



Ser Thr Glu Ile His Val Gly Phe Ala Gln Leu Thr Pro Pro Thr Pro

145                      150                      155                      160

Arg Gly Phe Pro Cys Thr

165

<210> 5

<211> 416

<212> PRT

<213> Homo sapiens

<400> 5

Met Ser Glu Ala Asp Gly Leu Arg Gln Arg Arg Pro Leu Arg Pro Gln

1                      5                      10                      15

Val Val Thr Asp Asp Asp Gly Gln Ala Pro Glu Ala Lys Asp Gly Ser

20                      25                      30

Ser Phe Ser Gly Arg Val Phe Arg Val Thr Phe Leu Met Leu Ala Val

35                      40                      45

Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu Leu Glu Ser Pro

50                      55                      60

Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro Leu Leu Leu Gly

65                      70                      75                      80

Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu Arg Leu Phe Glu

85                      90                      95

Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile Gly Asp Val Met

100                      105                      110

Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu Glu Asn Gly Glu  
115 120 125  
Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys Lys Thr Arg Asp  
130 135 140  
Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg Ala Gly Pro Asn  
145 150 155 160  
Gly Thr Leu Phe Val Ala Asp Ala Tyr Lys Gly Leu Phe Glu Val Asn  
165 170 175  
Pro Trp Lys Arg Glu Val Lys Leu Leu Leu Ser Ser Glu Thr Pro Ile  
180 185 190  
Glu Gly Lys Asn Met Ser Phe Val Asn Asp Leu Thr Val Thr Gln Asp  
195 200 205  
Gly Arg Lys Ile Tyr Phe Thr Asp Ser Ser Ser Lys Trp Gln Arg Arg  
210 215 220  
Asp Tyr Leu Leu Leu Val Met Glu Gly Thr Asp Asp Gly Arg Leu Leu  
225 230 235 240  
Glu Tyr Asp Thr Val Thr Arg Glu Val Lys Val Leu Leu Asp Gln Leu  
245 250 255  
Arg Phe Pro Asn Gly Val Gln Leu Ser Pro Ala Glu Asp Phe Val Leu  
260 265 270  
Val Ala Glu Thr Thr Met Ala Arg Ile Arg Arg Val Tyr Val Ser Gly  
275 280 285  
Leu Met Lys Gly Gly Ala Asp Leu Phe Val Glu Asn Met Pro Gly Phe  
290 295 300  
Pro Asp Asn Ile Arg Pro Ser Ser Ser Gly Gly Tyr Trp Val Gly Met

11

305                      310                      315                      320  
 Ser Thr Ile Arg Pro Asn Pro Gly Phe Ser Met Leu Asp Phe Leu Ser  
                          325                      330                      335  
 Glu Arg Pro Trp Ile Lys Arg Met Ile Phe Lys Leu Phe Ser Gln Glu  
                          340                      345                      350  
 Thr Val Met Lys Phe Val Pro Arg Tyr Ser Leu Val Leu Glu Leu Ser  
                          355                      360                      365  
 Asp Ser Gly Ala Phe Arg Arg Ser Leu His Asp Pro Asp Gly Leu Val  
                          370                      375                      380  
 Ala Thr Tyr Ile Ser Glu Val His Glu His Asp Gly His Leu Tyr Leu  
                          385                      390                      395                      400  
 Gly Ser Phe Arg Ser Pro Phe Leu Cys Arg Leu Ser Leu Gln Ala Val  
                          405                      410                      415

&lt;210&gt; 6

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Gly Ala Trp Ala  
                          1                      5                      10                      15  
 Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro  
                          20                      25                      30  
 Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu

12

35                      40                      45  
 Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Val Ser Pro Ser Pro  
 50                      55                      60  
 Leu Ser Pro Cys Pro Ala His Thr Pro Ser Gln Ala Arg Pro Leu His  
 65                      70                      75                      80  
 Pro Pro His Ile Pro Pro Pro Ala Phe Asp Pro Gln Ser Leu Pro Leu  
 85                      90                      95  
 Gly Ile Lys Pro Gln Met Gln Pro Phe Ile Tyr Ser Met Pro Gln Phe  
 100                      105                      110  
 Thr His Leu Pro Ala  
 115

&lt;210&gt; 7

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 7

Met Ser Val Glu Asp Gly Gly Met Pro Gly Leu Gly Arg Pro Arg Gln  
 1                      5                      10                      15  
 Ala Arg Trp Thr Leu Met Leu Leu Leu Ser Thr Ala Met Tyr Gly Ala  
 20                      25                      30  
 His Ala Pro Leu Leu Ala Leu Cys His Val Asp Gly Arg Val Pro Phe  
 35                      40                      45  
 Arg Pro Ser Ser Ala Val Leu Leu Thr Glu Leu Thr Lys Leu Leu Leu

50                      55                      60  
Cys Ala Phe Ser Leu Leu Val Gly Trp Gln Ala Trp Pro Gln Gly Pro  
65                      70                      75                      80  
Pro Pro Trp Arg Gln Ala Ala Pro Phe Ala Leu Ser Ala Leu Leu Tyr  
85                      90                      95  
Gly Ala Asn Asn Asn Leu Val Ile Tyr Leu Gln Arg Tyr Met Asp Pro  
100                      105                      110  
Ser Thr Tyr Gln Val Leu Ser Asn Leu Lys Ile Gly Ser Thr Ala Val  
115                      120                      125  
Leu Tyr Cys Leu Cys Leu Arg His Arg Leu Ser Val Arg Gln Gly Leu  
130                      135                      140  
Ala Leu Leu Leu Leu Met Ala Ala Gly Ala Cys Tyr Ala Ala Gly Gly  
145                      150                      155                      160  
Leu Gln Val Pro Gly Asn Thr Leu Pro Ser Pro Pro Pro Ala Ala Ala  
165                      170                      175  
Ala Ser Pro Met Pro Leu His Ile Thr Pro Leu Gly Leu Leu Leu Leu  
180                      185                      190  
Ile Leu Tyr Cys Leu Ile Ser Gly Leu Ser Ser Val Tyr Thr Glu Leu  
195                      200                      205  
Leu Met Lys Arg Gln Arg Leu Pro Leu Ala Leu Gln Asn Leu Phe Leu  
210                      215                      220  
Tyr Thr Phe Gly Val Leu Leu Asn Leu Gly Leu His Ala Gly Gly Gly  
225                      230                      235                      240  
Ser Gly Pro Gly Leu Leu Glu Gly Phe Ser Gly Trp Ala Ala Leu Val  
245                      250                      255

Val Leu Ser Gln Ala Leu Asn Gly Leu Leu Met Ser Ala Val Met Lys

260 265 270

His Gly Ser Ser Ile Thr Arg Leu Phe Val Val Ser Cys Ser Leu Val

275 280 285

Val Asn Ala Val Leu Ser Ala Val Leu Leu Arg Leu Gln Leu Thr Ala

290 295 300

Ala Phe Phe Leu Ala Thr Leu Leu Ile Gly Leu Ala Met Arg Leu Tyr

305 310 315 320

Tyr Gly Ser Arg

<210> 8

<211> 137

<212> PRT

<213> Homo sapiens

<400> 8

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu

1 5 10 15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu

20 25 30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser

35 40 45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro

50 55 60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln

15

65                      70                      75                      80  
 Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr  
                          85                      90                      95  
 Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly  
                          100                      105                      110  
 Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala  
                          115                      120                      125  
 Tyr Met Asp Ala Pro Lys Ala Ala Leu  
                          130                      135

&lt;210&gt; 9

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly Ser  
                          1                      5                      10                      15  
 Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val Ala Ala  
                          20                      25                      30  
 Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln  
                          35                      40                      45  
 Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His  
                          50                      55                      60  
 Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val

65	70	75	80
Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp			
85	90	95	
Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser His Asp			
100	105	110	
Leu Ala Gln Arg His Gly Leu Glu Ser Ala Ser Asp His His Gly Asn			
115	120	125	
Phe Ser Ile Thr Met Arg Asn Leu Thr Leu Leu Asp Ser Gly Leu Tyr			
130	135	140	
Cys Cys Leu Val Val Glu Ile Arg His His His Ser Glu His Arg Val			
145	150	155	160
His Gly Ala Met Glu Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser			
165	170	175	
Asn Cys Val Val Tyr Pro Ser Ser Ser Gln Glu Ser Glu Asn Ile Thr			
180	185	190	
Ala Ala Ala Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu			
195	200	205	
Pro Leu Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn			
210	215	220	
Arg Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile			
225	230	235	240
Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro Glu			
245	250	255	
Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln Pro Ser			
260	265	270	



Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro Leu Ser Pro

275

280

285

Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp Pro Val Pro Asp

290

295

300

Ser Pro Asn Phe Glu Val Ile

305

310

&lt;210&gt; 10

&lt;211&gt; 543

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 10

Met Ala Val Ser Glu Arg Arg Gly Leu Gly Arg Gly Ser Pro Ala Glu

1

5

10

15

Trp Gly Gln Arg Leu Leu Leu Val Leu Leu Leu Gly Gly Cys Ser Gly

20

25

30

Arg Ile His Arg Leu Ala Leu Thr Gly Glu Lys Arg Ala Asp Ile Gln

35

40

45

Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val Glu Leu

50

55

60

Ser Val Leu Arg Leu Gly Leu Arg Glu Ala Glu Glu Lys Ser Leu Leu

65

70

75

80

Val Gly Phe Ser Leu Ser Arg Val Arg Ser Gly Arg Val Arg Ser Tyr

85

90

95

Ser Thr Arg Asp Phe Gln Asp Cys Pro Leu Gln Lys Asn Ser Ser Ser

100 105 110

Phe Leu Val Leu Phe Leu Ile Asn Thr Lys Asp Leu Gln Val Gln Val

115 120 125

Arg Lys Tyr Gly Glu Gln Lys Thr Leu Phe Ile Phe Pro Gly Leu Leu

130 135 140

Pro Glu Ala Pro Ser Lys Pro Gly Leu Pro Lys Pro Gln Ala Thr Val

145 150 155 160

Pro Arg Lys Val Asp Gly Gly Gly Thr Ser Ala Ala Ser Lys Pro Lys

165 170 175

Ser Thr Pro Ala Val Ile Gln Gly Pro Ser Gly Lys Asp Lys Asp Leu

180 185 190

Val Leu Gly Leu Ser His Leu Asn Asn Ser Tyr Asn Phe Ser Phe His

195 200 205

Val Val Ile Gly Ser Gln Ala Glu Glu Gly Gln Tyr Ser Leu Asn Phe

210 215 220

His Asn Cys Asn Asn Ser Val Pro Gly Lys Glu His Pro Phe Asp Ile

225 230 235 240

Thr Val Met Ile Arg Glu Lys Asn Pro Asp Gly Phe Leu Ser Ala Ala

245 250 255

Glu Met Pro Leu Phe Lys Leu Tyr Met Val Met Ser Ala Cys Phe Leu

260 265 270

Ala Ala Gly Ile Phe Trp Val Ser Ile Leu Cys Arg Asn Thr Tyr Ser

275 280 285

Val Phe Lys Ile His Trp Leu Met Ala Ala Leu Ala Phe Thr Lys Ser

290 295 300  
Ile Ser Leu Leu Phe His Ser Ile Asn Tyr Tyr Phe Ile Asn Ser Gln  
305 310 315 320  
Gly His Pro Ile Glu Gly Leu Ala Val Met Tyr Tyr Ile Ala His Leu  
325 330 335  
Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala Leu Ile Gly Ser Gly  
340 345 350  
Trp Ala Phe Ile Lys Tyr Val Leu Ser Asp Lys Glu Lys Lys Val Phe  
355 360 365  
Gly Ile Val Ile Pro Met Gln Val Leu Ala Asn Val Ala Tyr Ile Ile  
370 375 380  
Ile Glu Ser Arg Glu Glu Gly Ala Ser Asp Tyr Val Leu Trp Lys Glu  
385 390 395 400  
Ile Leu Phe Leu Val Asp Leu Ile Cys Cys Gly Ala Ile Leu Phe Pro  
405 410 415  
Val Val Trp Ser Ile Arg His Leu Gln Asp Ala Ser Gly Thr Asp Gly  
420 425 430  
Lys Val Ala Val Asn Leu Ala Lys Leu Lys Leu Phe Arg His Tyr Tyr  
435 440 445  
Val Met Val Ile Cys Tyr Val Tyr Phe Thr Arg Ile Ile Ala Ile Leu  
450 455 460  
Leu Gln Val Ala Val Pro Phe Gln Trp Gln Trp Leu Tyr Gln Leu Leu  
465 470 475 480  
Val Glu Gly Ser Thr Leu Ala Phe Phe Val Leu Thr Gly Tyr Lys Phe  
485 490 495

Gln Pro Thr Gly Asn Asn Pro Tyr Leu Gln Leu Pro Gln Glu Asp Glu

500

505

510

Glu Asp Val Gln Met Glu Gln Val Met Thr Asp Ser Gly Phe Arg Glu

515

520

525

Gly Leu Ser Lys Val Asn Lys Thr Ala Ser Gly Arg Glu Leu Leu

530

535

540

&lt;210&gt; 11

&lt;211&gt; 1017

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 11

atgtctccat ccccgaccgc cctctctgt cttgggtgt gtctggggcg tgtgccagcg	60
cagagtggac cgtccccaa gccctccctc caggtcttgc ccagctccct ggtgcccctg	120
gagaagccag tgacctccg gtgccaggga cctccggcg tggacctgta ccgcctggag	180
aagctgagtt ccagcaggta ccaggatcag gcagtcctct tcatcccggc catgaagaga	240
agtctggctg gacgtaccg ctgtccctac cagaacggaa gcctctggtc cctgcccagc	300
gaccagctgg agctcgttgc caegggagtt ttgccaac cctcgtctc agcccagccc	360
ggcccggcgg tgcgtcagg aggggacgta accctacagt gtcagactcg gtatggcttt	420
gaccaatttg ctctgtacaa ggaaggggac cctgcgcctt acaagaatcc cgagagatgg	480
taccgggcta gtttcccat catcacgtg accgccgcc acagcggaac ctaccgatgc	540
tacagcttct ccagcaggga ccatacctg tggtcggccc ccagcagccc cctggagctt	600
gtggtcacag gaacctctgt gacccccagc cggttaccaa cagaaccacc ttctctgta	660
gcagaattct cagaagccac cgtgaactg accgtctcat tcacaaacga agtcttcaca	720

actgagactt ctaggagtat caccgccagt ccaaaggagt cagactctcc agctggteet 780  
 gcccgccagt actacaccaa gggcaacctg gtcgggatat gcctcggggc tgtgaccta 840  
 ataatcctgg cggggtttct ggcagaggac tggcacagcc ggaggaagcg cctgcggcac 900  
 aggggcaggg ctgtgcagag gccgttccg cccctccgc cccctccgct gacccggaaa 960  
 tcacacgggg gtcaggatgg agggcgacag gatgttcaca gccgcgggtt atgttca 1017

<210> 12

<211> 1461

<212> DNA

<213> Homo sapiens

<400> 12

atggcgteet cagcggaggg ggacgagggg actgtggtgg cgtcggcggg ggttctgcag 60  
 tcgggtttcc aggagctgag ccttaacaag ttggcgacgt cctcggcgcc gtcagaacag 120  
 gcgctgcggc tgatcatctc catcttcccg ggttaccctt ttgctttgtt ttatcggeat 180  
 taccttttct acaaggagac ctacctatc caccctctcc atacctttac aggcctctca 240  
 attgcttatt ttaactttgg aaaccagctc taccactccc tgctgtgtat tgtgcttcag 300  
 ttctcatcc ttgcactaat ggcccgacc atcactgccg tctcactac cttttgcttc 360  
 cagatggcct accttctggc tggatactat tacactgcc cggcaacta cgatatcaag 420  
 tggacaatgc cacatttgtt tctgactttg aagctgattg gtttggtgt tgactacttt 480  
 gacggagggg aagatcagaa ttcttgtcc tctgagcaac agaaatatgc catacgtggt 540  
 gtctcttccc tgcctggaagt tgctggtttc tctacttct atggggcctt cttggtaggg 600  
 cccagttct caatgaatca ctacatgaag ctggtgcagg gagagctgat tgacatacca 660  
 ggaaagatac caaacagcat cattctgct ctcaagcgcc tgagtctggg cttttctac 720  
 ctagtgggct acacactgct cagccccac atcacagaag actatctct cactgaagac 780

tatgacaacc acccccttctg gtcccgctgc atgtacatgc tgatctgggg caagtttgtg 840  
 ctgtacaaat atgtcacctg ttggtgggc acagaaggag tatgcatttt gacgggacctg 900  
 ggcttcaatg gctttgaaga aaagggaag gcaaagtggg atgacctgctg caacatgaag 960  
 gtgtggctct ttgaaacaaa ccccgcttc actggcacca ttgcctcatt caacatcaac 1020  
 accaagcctt ggggtggccc ctacatcttc aaacgactca agttccttgg aaataaagaa 1080  
 ctctctcagg gtctctcgtt gctattcctg gccctctggc acggcctgca ctccaggatac 1140  
 ctggctctgt tccagatgga attcctcatt gttattgttg aaagacaggc tgccagcttc 1200  
 attcaagaga gcccaccctt gagcaagctg gccgccattt ctgtctctca gccctctac 1260  
 tatttggctg aacagaccat ccactggctc ttcatgggtt actccatgac tgccttctgc 1320  
 ctcttcacgt gggacaaatg gcttaagggt tataaatcca tctatttctt tgccacatc 1380  
 ttcttctga gctactatt catattgctt tatattcaca aagcaatggt gcccaaggaaa 1440  
 gagaagttaa agaagatgga a 1461

&lt;210&gt; 13

&lt;211&gt; 786

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 13

atggcgagcag ccagcgctgg ggcaaccggg ctgtctctgc tcttctgat ggcggtagca 60  
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&lt;210&gt; 14

&lt;211&gt; 498

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

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 gaggtgagca ggagcactga gattcatgtg ggttttgcgc agctaaccac gccgaccca 480  
 cgcggttttc cctgcaca 498

&lt;210&gt; 15

&lt;211&gt; 1248

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 15

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gatgggctgg tggccacctt cctcagcgag gtgcacgaac acgatgggca cctgtacctg 1200  
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<210> 16

<211> 351

<212> DNA

<213> Homo sapiens

<400> 16

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tcagccaca tgccgctca cctgcgtgt gatgctgca gagctgtgga ttaccaggig 180  
agtccttcac cactgtcacc ctgcctgtct cacacccctt ctcagccag accctccac 240  
ccacctcaca ttccaccacc ggcctttgat cccaatccc taccactggg catcaagcca 300  
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<210> 17

<211> 972

<212> DNA

<213> Homo sapiens

<400> 17

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catgtggacg gccgagtgc cttccggccc tctcagccg tctgtgtgac tgagctgacc 180

aagctactgt tatgcgcctt ctccttctg gtaggtggc aagcatggcc ccaggggccc 240  
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 aacctggiga tctatcttca ggtttacatg gacccagca cctaccaggt gctgagtaat 360  
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 tatggcagcc gc 972

&lt;210&gt; 18

&lt;211&gt; 411

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 18

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 ccggttgtca ccaccaccac atccaccact gtggtgcatg ccccttatcc tcagctcca 180  
 agtgtgcgc ccagctacc tggaccaagc taccagggt accacaccat gccgctcag 240

ccagggatgc cagcagcacc ctaccaatg cagtaccac cacttacc agcccagccc 300  
 atgggcccac cggectacca cgagacctg gctggaggag cagccgcgcc ctaccccgcc 360  
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<210> 19

<211> 933

<212> DNA

<213> Homo sapiens

<400> 19

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 ctgtatgtct gtcccgagg gcagaacgt accctcacct gcaggctctt gggcctgtg 180  
 gacaaagggc acgatgtgac ctctacaag acgtggtacc gcagctcgag gggcgaggtg 240  
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 tggcctccg accaccatgg caactctcc atcccatgc gcaacctgac cctgctggat 420  
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<210> 20

<211> 1629

<212> DNA

<213> Homo sapiens

<400> 20

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gaggtggagt tgagcgtcct gcggctgggc ctccgggagg cagaagagaa gtcctctgt	240
gtggggttca gtctcagcgg ggttcggctt ggcagagtgc gctctattc aaccgggat	300
ttccaggact gccctctcca gaaaaacagt agcagtttcc tggctctgtt cctcatcaac	360
accaaggatc tgcaggctca ggtgcggaag tatggagagc agaagacgtt gtttatctt	420
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ccccgcaagg tggatggcgg agggacctct gcagccagca agcccaagtc aacaccgca	540
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<210> 21

<211> 2007

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (46)... (1065)

<400> 21

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54

Met Ser Pro

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 Ser Pro Thr Ala Leu Phe Cys Leu Gly Leu Cys Leu Gly Arg Val Pro  
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 gcg cag agt gga ccg ctc ccc aag ccc tcc ctc cag gct ctg ccc agc 150  
 Ala Gln Ser Gly Pro Leu Pro Lys Pro Ser Leu Gln Ala Leu Pro Ser  
 20 25 30 35  
 tcc ctg gtg ccc ctg gag aag cca gtg acc ctc cgg tgc cag gga cct 198  
 Ser Leu Val Pro Leu Glu Lys Pro Val Thr Leu Arg Cys Gln Gly Pro  
 40 45 50  
 ccg gcc gtg gac ctg tac cgc ctg gag aag ctg agt tcc agc agg tac 246  
 Pro Gly Val Asp Leu Tyr Arg Leu Glu Lys Leu Ser Ser Ser Arg Tyr  
 55 60 65  
 cag gat cag gca gtc ctc ttc atc ccg gcc atg aag aga agt ctg gct 294  
 Gln Asp Gln Ala Val Leu Phe Ile Pro Ala Met Lys Arg Ser Leu Ala  
 70 75 80  
 gga cgc tac cgc tgc tcc tac cag aac gga agc ctc tgg tcc ctg ccc 342  
 Gly Arg Tyr Arg Cys Ser Tyr Gln Asn Gly Ser Leu Trp Ser Leu Pro  
 85 90 95  
 agc gac cag ctg gag ctc gtt gcc acg gga gtt ttt gcc aaa ccc tcg 390  
 Ser Asp Gln Leu Glu Leu Val Ala Thr Gly Val Phe Ala Lys Pro Ser  
 100 105 110 115  
 ctc tca gcc cag ccc gcc ccg gcg gtg tgc tca gga ggg gac gta acc 438  
 Leu Ser Ala Gln Pro Gly Pro Ala Val Ser Ser Gly Gly Asp Val Thr  
 120 125 130  
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Leu Gln Cys Gln Thr Arg Tyr Gly Phe Asp Gln Phe Ala Leu Tyr Lys  
 135 140 145  
 gaa ggg gac cct gcg ccc tac aag aat ccc gag aga tgg tac cgg gct 534  
 Glu Gly Asp Pro Ala Pro Tyr Lys Asn Pro Glu Arg Trp Tyr Arg Ala  
 150 155 160  
 agt ttt ccc atc atc acg gtg acc gcc gcc cac agc gga acc tac cga 582  
 Ser Phe Pro Ile Ile Thr Val Thr Ala Ala His Ser Gly Thr Tyr Arg  
 165 170 175  
 tgc tac agc ttc tcc agc agg gac cca tac ctg tgg tgg gcc ccc agc 630  
 Cys Tyr Ser Phe Ser Ser Arg Asp Pro Tyr Leu Trp Ser Ala Pro Ser  
 180 185 190 195  
 gac ccc ctg gag ctt gtg gtc aca gga acc tct gtg acc ccc agc cgg 678  
 Asp Pro Leu Glu Leu Val Val Thr Gly Thr Ser Val Thr Pro Ser Arg  
 200 205 210  
 tta cca aca gaa cca cct tcc tgg gta gca gaa ttc tca gaa gcc acc 726  
 Leu Pro Thr Glu Pro Pro Ser Ser Val Ala Glu Phe Ser Glu Ala Thr  
 215 220 225  
 gct gaa ctg acc gtc tca ttc aca aac gaa gtc ttc aca act gag act 774  
 Ala Glu Leu Thr Val Ser Phe Thr Asn Glu Val Phe Thr Thr Glu Thr  
 230 235 240  
 tct agg agt atc acc gcc agt cca aag gag tca gac tct cca gct ggt 822  
 Ser Arg Ser Ile Thr Ala Ser Pro Lys Glu Ser Asp Ser Pro Ala Gly  
 245 250 255  
 cct gcc cgc cag tac tac acc aag ggc aac ctg gtc cgg ala tgc ctc 870  
 Pro Ala Arg Gln Tyr Tyr Thr Lys Gly Asn Leu Val Arg Ile Cys Leu

260	265	270	275	
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Gly Ala Val Ile Leu Ile Ile Leu Ala Gly Phe Leu Ala Glu Asp Trp				
	280	285	290	
cac agc cgg agg aag cgc ctg cgg cac agg ggc agg gct gtg cag agg				966
His Ser Arg Arg Lys Arg Leu Arg His Arg Gly Arg Ala Val Gln Arg				
295		300	305	
ccg ctt cgg ccc ctc ccg ccc ctc ccg ctg acc cgg aaa tca cac ggg				1014
Pro Leu Pro Pro Leu Pro Pro Leu Pro Leu Thr Arg Lys Ser His Gly				
310		315	320	
ggt cag gat gga ggc cga cag gat gtt cac agc cgc ggg tta tgt tca				1062
Gly Gln Asp Gly Gly Arg Gln Asp Val His Ser Arg Gly Leu Cys Ser				
325		330	335	
tgaccgct gaaccccagg caccgtcgta tccaagggag ggcacatggc atgggagggc				1120
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<210> 22

<211> 2264

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (85)... (1548)

<400> 22

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 Met Ala Ser Ser Ala Glu Gly Asp Glu

1

5

ggg act gtg gtg gcg ctg gcg ggg gtt ctg cag tcc ggt ttc cag gag 159  
 Gly Thr Val Val Ala Leu Ala Gly Val Leu Gln Ser Gly Phe Gln Glu

10

15

20

25

ctg agc ctt aac aag ttg gcg acg tcc ctg ggc gcg tca gaa cag gcg 207  
 Leu Ser Leu Asn Lys Leu Ala Thr Ser Leu Gly Ala Ser Glu Gln Ala

30

35

40

ctg cgg ctg atc atc tcc atc ttc ctg ggt tac ccc ttt gct ttg ttt 255  
 Leu Arg Leu Ile Ile Ser Ile Phe Leu Gly Tyr Pro Phe Ala Leu Phe  
 45 50 55  
 tat cgg cat tac ctt ttc tac aag gag acc tac ctc atc cac ctc ttc 303  
 Tyr Arg His Tyr Leu Phe Tyr Lys Glu Thr Tyr Leu Ile His Leu Phe  
 60 65 70  
 cat acc ttt aca ggc ctc tca att gct tat ttt aac ttt gga aac cag 351  
 His Thr Phe Thr Gly Leu Ser Ile Ala Tyr Phe Asn Phe Gly Asn Gln  
 75 80 85  
 ctc tac cac tcc ctg ctg tgt att gtg ctt cag ttc ctc atc ctt cga 399  
 Leu Tyr His Ser Leu Leu Cys Ile Val Leu Gln Phe Leu Ile Leu Arg  
 90 95 100 105  
 cta atg ggc cgc acc atc act gcc gtc ctc act acc ttt tgc ttc cag 447  
 Leu Met Gly Arg Thr Ile Thr Ala Val Leu Thr Thr Phe Cys Phe Gln  
 110 115 120  
 atg gcc tac ctt ctg gct gga tac tat tac act gcc acc ggc aac tac 495  
 Met Ala Tyr Leu Leu Ala Gly Tyr Tyr Tyr Thr Ala Thr Gly Asn Tyr  
 125 130 135  
 gat atc aag tgg aca atg cca cat tgt gtt ctg act ttg aag ctg att 543  
 Asp Ile Lys Trp Thr Met Pro His Cys Val Leu Thr Leu Lys Leu Ile  
 140 145 150  
 ggt ttg gct gtt gac tac ttt gac gga ggg aaa gat cag aat tcc ttg 591  
 Gly Leu Ala Val Asp Tyr Phe Asp Gly Gly Lys Asp Gln Asn Ser Leu  
 155 160 165  
 tcc tct gag caa cag aaa tat gcc ata cgt ggt gtt cct tcc ctg ctg 639

Ser Ser Glu Gln Gln Lys Tyr Ala Ile Arg Gly Val Pro Ser Leu Leu

170 175 180 185

gaa gtt gct ggt ttc tcc tac ttc tat ggg gcc ttc ttg gta ggg ccc 687

Glu Val Ala Gly Phe Ser Tyr Phe Tyr Gly Ala Phe Leu Val Gly Pro

190 195 200

cag ttc tca atg aat cac tac atg aag ctg gtg cag gga gag ctg att 735

Gln Phe Ser Met Asn His Tyr Met Lys Leu Val Gln Gly Glu Leu Ile

205 210 215

gac ata cca gga aag ata cca aac agc atc att cct gct ctc aag cgc 783

Asp Ile Pro Gly Lys Ile Pro Asn Ser Ile Ile Pro Ala Leu Lys Arg

220 225 230

ctg agt ctg ggc ctt ttc tac cta gtg ggc tac aca ctg ctc agc ccc 831

Leu Ser Leu Gly Leu Phe Tyr Leu Val Gly Tyr Thr Leu Leu Ser Pro

235 240 245

cac atc aca gaa gac tat ctc ctc act gaa gac tat gac aac cac ccc 879

His Ile Thr Glu Asp Tyr Leu Leu Thr Glu Asp Tyr Asp Asn His Pro

250 255 260 265

ttc tgg ttc cgc tgc atg tac atg ctg atc tgg ggc aag ttt gtg ctg 927

Phe Trp Phe Arg Cys Met Tyr Met Leu Ile Trp Gly Lys Phe Val Leu

270 275 280

tac aaa tat gtc acc tgt tgg ctg gtc aca gaa gga gta tgc att ttg 975

Tyr Lys Tyr Val Thr Cys Trp Leu Val Thr Glu Gly Val Cys Ile Leu

285 290 295

acg ggc ctg ggc ttc aat ggc ttt gaa gaa aag ggc aag gca aag tgg 1023

Thr Gly Leu Gly Phe Asn Gly Phe Glu Glu Lys Gly Lys Ala Lys Trp

300	305	310	
gat gcc tgt gcc aac atg aag gtg tgg ctc ttt gaa aca aac ccc cgc			1071
Asp Ala Cys Ala Asn Met Lys Val Trp Leu Phe Glu Thr Asn Pro Arg			
315	320	325	
ttc act ggc acc att gcc tca ttc aac atc aac acc aac gcc tgg gtg			1119
Phe Thr Gly Thr Ile Ala Ser Phe Asn Ile Asn Thr Asn Ala Trp Val			
330	335	340	345
gcc cgc tac atc ttc aaa cga ctc aag ttc ctt gga aat aaa gaa ctc			1167
Ala Arg Tyr Ile Phe Lys Arg Leu Lys Phe Leu Gly Asn Lys Glu Leu			
350	355	360	
tct cag ggt ctc tgg ttg cta ttc ctg gcc ctc tgg cac ggc ctg cac			1215
Ser Gln Gly Leu Ser Leu Leu Phe Leu Ala Leu Trp His Gly Leu His			
365	370	375	
tea gga tac ctg gtc tgc ttc cag atg gaa ttc ctc att gtt att gtg			1263
Ser Gly Tyr Leu Val Cys Phe Gln Met Glu Phe Leu Ile Val Ile Val			
380	385	390	
gaa aga cag gct gcc agg ctc att caa gag agc ccc acc ctg agc aag			1311
Glu Arg Gln Ala Ala Arg Leu Ile Gln Glu Ser Pro Thr Leu Ser Lys			
395	400	405	
ctg gcc gcc att act gtc ctc cag ccc ttc tac tat ttg gtg caa cag			1359
Leu Ala Ala Ile Thr Val Leu Gln Pro Phe Tyr Tyr Leu Val Gln Gln			
410	415	420	425
acc atc cac tgg ctc ttc atg ggt tac tcc atg act gcc ttc tgc ctc			1407
Thr Ile His Trp Leu Phe Met Gly Tyr Ser Met Thr Ala Phe Cys Leu			
430	435	440	

ttc acg tgg gac aaa tgg ctt aag gtg tat aaa tcc atc tat ttc ctt 1455  
 Phe Thr Trp Asp Lys Trp Leu Lys Val Tyr Lys Ser Ile Tyr Phe Leu  
 445 450 455  
 ggc cac atc ttc ttc ctg agc cta cta ttc ata ttg cct tat att cac 1503  
 Gly His Ile Phe Phe Leu Ser Leu Leu Phe Ile Leu Pro Tyr Ile His  
 460 465 470  
 aaa gca atg gtg cca agg aaa gag aag tta aag aag atg gaa taatc 1550  
 Lys Ala Met Val Pro Arg Lys Glu Lys Leu Lys Lys Met Glu  
 475 480 485  
 catttcctg gtggcctgtg cgggaactggt gcagaaacta ctgctctccc ttttcacagc 1610  
 actcctttgc ccagagcag agaatggaaa agccaggag gtggaagatc gatgcttcca 1670  
 gctglcctc tgcctccagc caagtcttca ttggggcca aaggggaaac tttttttgg 1730  
 agaaggcgtc ttgctttgtc acccagctg gaatgcagtg ggggatctc agctcacgc 1790  
 aacctccacc tctgggttc aagtgatttt cctgcctcag cctcccaagt agctgggaat 1850  
 acaggcacgc caccatgccc agctaatttt tgtattttca gtagaaacgg gatttcacca 1910  
 cgttggccag gctggctctg aactcctgac cgcaagtgat ccaccgcct ccgcctccca 1970  
 aagtgtctggg attacaggcg tgagccaccg tgcctggccc aaaggggaaa ctctgttggg 2030  
 aggagcagag gggctcacat ctccctctg attccccat gcacattgcc ttatctctc 2090  
 ccatctagcc aggaatctat tgtgttttc ttctgccaat ttactatgat tgtgtatgtg 2150  
 ccgtlaccac cccccccc atgggggggt ggagagggt gcaaggcct gcctgtccca 2210  
 cttttctac cttggaactg tattagataa aatcattct gttgttcag tttt 2264

&lt;210&gt; 23

&lt;211&gt; 1907

&lt;212&gt; DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (35)... (823)

<400> 23

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Met Ala Ala Ala Ser Ala	
1 5	
ggg gca acc cgg ctg ctc ctg ctc ttg ctg atg gcg gta gca gcg ccc	100
Gly Ala Thr Arg Leu Leu Leu Leu Leu Met Ala Val Ala Ala Pro	
10 15 20	
agt cga gcc cgg ggc agc ggc tgc cgg gcc ggg act ggt gcg cga ggg	148
Ser Arg Ala Arg Gly Ser Gly Cys Arg Ala Gly Thr Gly Ala Arg Gly	
25 30 35	
gct ggg gcg gaa ggt cga gag ggc gag gcc tgt ggc acg gtg ggg ctg	196
Ala Gly Ala Glu Gly Arg Glu Gly Glu Ala Cys Gly Thr Val Gly Leu	
40 45 50	
ctg ctg gag cac tca ttt gag atc gat gac agt gcc aac ttc cgg aag	244
Leu Leu Glu His Ser Phe Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys	
55 60 65 70	
cgg ggc tca ctg ctc tgg aac cag cag gat ggt acc ttg tcc ctg tca	292
Arg Gly Ser Leu Leu Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser	
75 80 85	

cag cgg cag ctc agc gag gag gag cgg ggc cga ctc cgg gat gtg gca 340  
 Gln Arg Gln Leu Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala  
 90 95 100  
 gcc ctg aat ggc ctg tac cgg gtc cgg atc cca agg cga ccc ggg gcc 388  
 Ala Leu Asn Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala  
 105 110 115  
 ctg gat ggc ctg gaa gct ggt ggc tat gtc tcc tcc ttt gtc cct gcg 436  
 Leu Asp Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala  
 120 125 130  
 tgc tcc ctg gtg gag tgc cac ctg tgc gac cag ctg acc ctg cac gtg 484  
 Cys Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val  
 135 140 145 150  
 gat gtg gcc ggc aac gtg gtg ggc gtg tgc gtg gtg acg cac ccc ggg 532  
 Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro Gly  
 155 160 165  
 ggc tgc cgg ggc cat gag gtg gag gac gtg gac ctg gag ctg ttc aac 580  
 Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu Phe Asn  
 170 175 180  
 acc tgc gtg cag ctg cag ccg ccc acc aca gcc cca ggc cct gag acg 628  
 Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly Pro Glu Thr  
 185 190 195  
 gcg gcc ttc att gag cgc ctg gag atg gaa cag gcc cag aag gcc aag 676  
 Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala Gln Lys Ala Lys  
 200 205 210  
 aac ccc cag gag cag aag tcc ttc ttc gcc aaa tac tgg atg tac atc 724





atccatcatgt ggctgtgtgg agctcagctg tgttgtgtgg cagtttattt aactgtcccc 1900

cagatcg 1907

<210> 24

<211> 1727

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (20)... (520)

<400> 24

agccgggtgg ggctcggg atg cag ccg ccg gtg ccc ggg ccc ctg ggc 49

Met Gln Pro Pro Val Pro Gly Pro Leu Gly

1 5 10

ctg ctg gac ccc gca gaa ggg ctt tgc agg agg aag aag acg tgc ctc 97

Leu Leu Asp Pro Ala Glu Gly Leu Ser Arg Arg Lys Lys Thr Ser Leu

15 20 25

tgg ttt gtg ggg tct ctg ctg ctg gtg tcc gtc ctc ata gtc acc gtc 145

Trp Phe Val Gly Ser Leu Leu Leu Val Ser Val Leu Ile Val Thr Val

30 35 40

ggg ctg gct gcc acc acc agg acg gag aat gtg acc gtt ggg ggc tac 193

Gly Leu Ala Ala Thr Thr Arg Thr Glu Asn Val Thr Val Gly Gly Tyr

45 50 55

tac cca ggg atc att ctc ggc ttt gga tct ttc tta gga att att ggc 241  
 Tyr Pro Gly Ile Ile Leu Gly Phe Gly Ser Phe Leu Gly Ile Ile Gly  
 60 65 70  
 atc aac ttg gtg gag aat aga agg caa atg ctg gtg gca gcg atc gtg 289  
 Ile Asn Leu Val Glu Asn Arg Arg Gln Met Leu Val Ala Ala Ile Val  
 75 80 85 90  
 ttt atc agt ttt ggc gtg gtg gcc gcc ttc tgc tgc gcc atc gtg gac 337  
 Phe Ile Ser Phe Gly Val Val Ala Ala Phe Cys Cys Ala Ile Val Asp  
 95 100 105  
 ggc gta ttt gca gca cag cac att gaa ccg agg ccc ctc acc acg gga 385  
 Gly Val Phe Ala Ala Gln His Ile Glu Pro Arg Pro Leu Thr Thr Gly  
 110 115 120  
 aga tgc cag ttt tac tcc agt ggg gtg ggg tac ttg tac gat gtc tac 433  
 Arg Cys Gln Phe Tyr Ser Ser Gly Val Gly Tyr Leu Tyr Asp Val Tyr  
 125 130 135  
 cag aca gag gtg agc agg agc act gag att cat gtg ggt ttt gct cag 481  
 Gln Thr Glu Val Ser Arg Ser Thr Glu Ile His Val Gly Phe Ala Gln  
 140 145 150  
 cta acc ccg ccg acc cca cgc ggt ttt ccc tgc aca taggcgtggt ctg 530  
 Leu Thr Pro Pro Thr Pro Arg Gly Phe Pro Cys Thr  
 155 160 165  
 aatatttga ttctaatagt tcttgggggt cacccttga gctggtgaac cgttgatgcc 590  
 ccttgtgttt gggaccttga catttcgatg tgcgttatit cactctggag tcagagttct 650  
 ggacttgctt cattaaalca caacagtctc agagtgcacg tgtccagttc tgtatggctc 710  
 ttccaattag catlttttcta atttaattat tgcaataaga agcaaggata atacatttac 770

agtgtccgag aaacttctgg atttccctga gccaccgaca ggggcagltg gacctcattt 830  
 ctctttccag gtcacctgtc actccctgga cggcaagtgc cagctgaagg tgagaagcaa 890  
 cacctgttac tgctgtgacc tctatgcctg cgggagcgca gagccctcgc ccgcctacta 950  
 tgagttcacc ggctgcagcg gctgccagga cgtgtgcac ctgtaccgcc tgccttgggc 1010  
 ctctgcagtt ctgaacgtcc tgggcctglt cctgggcacc atcaccgccg ccgtccctggg 1070  
 ggccctcaag gacatgggtc ctcgtccca gctggcctat ggcccagccg tcccaccaca 1130  
 gacctctac aaccccgccc agcagatcct ggccctacga ggcttcgcc tgacgcccga 1190  
 gectgtcccg acctgtcgtt cctaccctct gcccttcag cctgcagcc gcttccagtt 1250  
 tgcgccctcc tctgccctgg cttcgtctga ggacctgcag ccacctctc caagcagctc 1310  
 tggctctggg ctcccgccc aggcctccac gtgctacga cccacctact ttccccggg 1370  
 ggagaagcca cccccctac caccctgata gaggcgtgga glaaaagata acttgtttgt 1430  
 tttttttaa aaaaaaaaag gcagcctcta gaaatccgc ttctgtggcc aacctccag 1490  
 agaaccggg agaagtgtcc agaagtctgt cccctcctt cctccctggg cacactggg 1550  
 aggagggctg gaaccaggca gggagtggg cctccagac ccaggctggt gacaccttg 1610  
 ctgggctct gctcacacca aatggcgctg aaagtccca cccggctcc tccctgaga 1670  
 gcaattgtt tgggtgtttc acatccctta attaattagc tattattatg attttgc 1727

<210> 25

<211> 2150

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (32)... (1282)

&lt;400&gt; 25

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Met Ser Glu Ala Asp Gly Leu	
1 5	
cga cag cgc cgg ccc ctg cgg ccg cag gtc gtc aca gac gat gat ggc	100
Arg Gln Arg Arg Pro Leu Arg Pro Gln Val Val Thr Asp Asp Asp Gly	
10 15 20	
cag gcc ccg gag gct aag gac ggc agc tcc ttt agc ggc aga gtt ttc	148
Gln Ala Pro Glu Ala Lys Asp Gly Ser Ser Phe Ser Gly Arg Val Phe	
25 30 35	
cga glg acc ttc ttg atg ctg gct gtt tct ctc acc gtt ccc ctg ctt	196
Arg Val Thr Phe Leu Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu	
40 45 50 55	
gga gcc atg atg ctg ctg gaa tct cct ata gat cca cag cct ctc agc	244
Gly Ala Met Met Leu Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser	
60 65 70	
ttc aaa gaa ccc ccg ctc ttg ctt ggt gtt ctg cat cca aat acg aag	292
Phe Lys Glu Pro Pro Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys	
75 80 85	
ctg cga cag gca gaa agg ctg ttt gaa aat caa ctt gtt gga ccg gag	340
Leu Arg Gln Ala Glu Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu	
90 95 100	
tcc ata gca cat att ggg gal gtg atg ttt act ggg aca gca gat ggc	388
Ser Ile Ala His Ile Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly	

105 110 115  
cgg gtc gta aaa ctt gaa aat ggt gaa ata gag acc att gcc cgg ttt 436  
Arg Val Val Lys Leu Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe  
120 125 130 135  
ggg tgc ggc cct tgc aaa acc cga gat gat gag cct gtg tgt ggg aga 484  
Gly Ser Gly Pro Cys Lys Thr Arg Asp Asp Glu Pro Val Cys Gly Arg  
140 145 150  
ccc ctg ggt atc cgt gca ggg ccc aat ggg act ctc ttt gtg gcc gat 532  
Pro Leu Gly Ile Arg Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp  
155 160 165  
gca tac aag gga cta ttt gaa gta aat ccc tgg aaa cgt gaa gtg aaa 580  
Ala Tyr Lys Gly Leu Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys  
170 175 180  
ctg ctg ctg tcc tcc gag aca ccc att gag ggg aag aac atg tcc ttt 628  
Leu Leu Leu Ser Ser Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe  
185 190 195  
gtg aat gat ctt aca gtc act cag gat ggg agg aag att tat ttc acc 676  
Val Asn Asp Leu Thr Val Thr Gln Asp Gly Arg Lys Ile Tyr Phe Thr  
200 205 210 215  
gat tct agc agc aaa tgg caa aga cga gac tac ctg ctt ctg gtg atg 724  
Asp Ser Ser Ser Lys Trp Gln Arg Arg Asp Tyr Leu Leu Leu Val Met  
220 225 230  
gag ggc aca gat gac ggg cgc ctg ctg gag tat gat act gtg acc agg 772  
Glu Gly Thr Asp Asp Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg  
235 240 245

gaa gta aaa gtt tta ttg gac cag ctg cgg ttc ccg aat gga gtc cag			820
Glu Val Lys Val Leu Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln			
250	255	260	
ctg tct cct gca gaa gac ttt gtc ctg gtg gca gaa aca acc atg gcc			868
Leu Ser Pro Ala Glu Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala			
265	270	275	
agg ata cga aga gtc tac gtt tct ggc ctg atg aag ggc ggg gct gat			916
Arg Ile Arg Arg Val Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp			
280	285	290	295
ctg ttt gtg gag aac atg cct gga ttt cca gac aac atc cgg ccc agc			964
Leu Phe Val Glu Asn Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser			
300	305	310	
agc tct ggg ggg tac tgg gtg ggc atg tgg acc atc cgc cct aac cct			1012
Ser Ser Gly Gly Tyr Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro			
315	320	325	
ggg ttt tcc atg ctg gat ttc tta tct gag aga ccc tgg att aaa agg			1060
Gly Phe Ser Met Leu Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg			
330	335	340	
atg att ttt aag ctc ttt agt caa gag acg gtg atg aag ttt gtg ccg			1108
Met Ile Phe Lys Leu Phe Ser Gln Glu Thr Val Met Lys Phe Val Pro			
345	350	355	
cgg tac agc ctc gtc cta gaa ctc agc gac agc ggt gcc ttc cgg aga			1156
Arg Tyr Ser Leu Val Leu Glu Leu Ser Asp Ser Gly Ala Phe Arg Arg			
360	365	370	375
agc ctg cat gat ccc gat ggg ctg gtg gcc acc tac atc agc gag gtg			1204

Ser Leu His Asp Pro Asp Gly Leu Val Ala Thr Tyr Ile Ser Glu Val

380

385

390

cac gaa cac gat ggg cac ctg tac ctg ggc tet ttc agg tcc ecc ttc 1252

His Glu His Asp Gly His Leu Tyr Leu Gly Ser Phe Arg Ser Pro Phe

395

400

405

ctc tgc aga ctc agc ctc cag gct gtt tagccctccc agatagctgc c 1300

Leu Cys Arg Leu Ser Leu Gln Ala Val

410

415

cctgccacgc aggccaggag tcttcacact caggcaccag gcctgggtcca ggaggagctg 1360

tggacacagt cgtgggtcaa gtgtccacat gcacctgtta gtccctgaga ggtgggtggga 1420

atggctgctt ccttctcga ggaagcccg gcccacctg ggcttgtctt tctgtttaga 1480

gggaagtgtg acatatctgc catgaggaac ataaattcat gtaaagccat tttctcttaa 1550

acaaaacaaa actttctaag tacagtcatt ctctaggatt tgggaagctc ctgtcacttg 1600

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tccatagtgt gtatgaaaag ctgtttgact ctacgggctc agagaggact ttgctgggtt 1900

tctttctgtg aatatctcgc tgcagaccat gctggaattg gatgattctg caattcggga 1960

cctactgcag gggtcggttt agtaacgtct tgcctgtgat ctttgttctt gacctctaga 2020

ccccagatg tgaacagtgc acgtgttaat gtcacttttg ctcatgtgtt ataagcccca 2080

agttgctgta tattttcaca agtatgtcta cacactggtc atgattttga taataaataa 2140

cgataaatcg 2150

&lt;211&gt; 1986

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (28)... (381)

&lt;400&gt; 26

acacttgctg aactggctcc tggggcc atg agg ctg tca ctg cca ctg ctg 51

Met Arg Leu Ser Leu Pro Leu Leu

1

5

ctg ctg ctg ctg gga gcc tgg gcc atc cca ggg ggc ctc ggg gac agg 99

Leu Leu Leu Leu Gly Ala Trp Ala Ile Pro Gly Gly Leu Gly Asp Arg

10

15

20

gcg cca ctc aca gcc aca gcc cca caa ctg gat gat gag gag atg tac 147

Ala Pro Leu Thr Ala Thr Ala Pro Gln Leu Asp Asp Glu Glu Met Tyr

25

30

35

40

tca gcc cac atg ccc gct cac ctg cgc tgt gat gcc tgc aga gct gtg 195

Ser Ala His Met Pro Ala His Leu Arg Cys Asp Ala Cys Arg Ala Val

45

50

55

gct tac cag gtg agt cct tca cca ctg tca ccc tgc cct gct cac acc 243

Ala Tyr Gln Val Ser Pro Ser Pro Leu Ser Pro Cys Pro Ala His Thr

60

65

70

cct tct caa gcc aga ccc ctc cac cca cct cac att cca cca ccg gcc 291



Pro Ser Gln Ala Arg Pro Leu His Pro Pro His Ile Pro Pro Pro Ala  
 75 80 85  
 ttt gat ccc caa tcc cta cca ctg ggc atc aag cca cag atg cag cct 339  
 Phe Asp Pro Gln Ser Leu Pro Leu Gly Ile Lys Pro Gln Met Gln Pro  
 90 95 100  
 ttc ata tat tcc atg cct cag ttt acc cat ctg cct gcc ta 380  
 Phe Ile Tyr Ser Met Pro Gln Phe Thr His Leu Pro Ala  
 105 110 115  
 acagcagaca atctgggaga cctcctcagt attttgagac cccaggaat cactcacttg 440  
 tccttagact tctcccttcc caggcccatc cttagtcg gactccctcc ccaacctga 500  
 cggggcggct ttggctatgt gtacatggcg caagtgcaca cgtgtgagcg cctgcacgtg 560  
 agtatgcgtg tgtctggctt cacacacaca cctgtcgagc atgcctgcgt gccagtgtct 620  
 ctgtgaggtg ggggcctggg agtacttggt tgattgaata ttgggtccca gttttctta 680  
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 tggcacatac ctgtagtccc agctacctgg gaggtgagg gagaagaatc acttgaacct 920  
 gggagggtgga ggctgcagtg agctgagatc gtaccactgc actccagcct gggcgacgaa 980  
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 gcagggtgic cctggacgag ggaccccagt gcccaggcct cacctaccac ttcagcattt 1100  
 ctttcccatc cccaccccc atcccagaga gctttggggg ctgggggagg ggccatgcaa 1160  
 cagcctcaca ggtgcttctt gctcaaacgg ctctcttgcc actttatttt ccccagagac 1220  
 tctgtccta tctcccccac ctcccctaa ctgagcagca gtctgagge cctgcctccc 1280  
 agtccctctt tgttcagat gtggcaaat ctggcaagg cagagaccaa acttcatacc 1340  
 tcaaactctg gggggcggcg ggagctgagc gagtgtgtct acacggatgt cctggaccgg 1400

agctgctccc ggaactggca ggactacgga gttegagaag tggaccaagt gaaacgtctc 1460  
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 ccttgcccta ccaggtgatg cccggggctt ggggatagga tgaagtcctt ggagccttgg 1580  
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 caaggccgag gggtcttggg ggcattgcta tgtgggggac cccagggggc ctgctcagag 1760  
 aaggtgtcag ccacaagaga agagctctag tcttggaact taccctctct tgaagaagc 1820  
 tggggcttgc tctgacggc tccactcccg tctgcaggca gccaggaggc caggaagccc 1880  
 ttgtctgtg ctgccatctt gctccctcc tccagctca gggcaactcg gcctgggttg 1940  
 gagtcaacgc ctccctctt ggactcaaat aaaacccagt gacctc 1986

<210> 27

<211> 2170

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (241)... (1215)

<400> 27

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 gtattctctc tggcaatggt ccacggcttc tcttctctgg gagctggctc cataactga 180  
 ttttcccaa acgtgttgca atccctgctg ccccttagcc acccagggtc ttgtgtgggt 240

atg agt gta gag gat ggg ggt atg cca ggc ctg ggc cgt ccc agg cag 288  
 Met Ser Val Glu Asp Gly Gly Met Pro Gly Leu Gly Arg Pro Arg Gln  
 1 5 10 15  
 gcc cgc tgg acc ctg atg cta ctc cta tcc act gcc atg tac ggt gcc 336  
 Ala Arg Trp Thr Leu Met Leu Leu Leu Ser Thr Ala Met Tyr Gly Ala  
 20 25 30  
 cat gcc cca ttg ctg gca ctg tgc cat gtg gac ggc cga gtg ccc ttc 384  
 His Ala Pro Leu Leu Ala Leu Cys His Val Asp Gly Arg Val Pro Phe  
 35 40 45  
 cgg ccc tcc tca gcc gtg ctg ctg act gag ctg acc aag cta ctg tta 432  
 Arg Pro Ser Ser Ala Val Leu Leu Thr Glu Leu Thr Lys Leu Leu Leu  
 50 55 60  
 tgc gcc ttc tcc ctt ctg gta ggc tgg caa gca tgg ccc cag ggg ccc 480  
 Cys Ala Phe Ser Leu Leu Val Gly Trp Gln Ala Trp Pro Gln Gly Pro  
 65 70 75 80  
 cca ccc tgg cgc cag gct gct ccc ttc gca cta tca gcc ctg ctc tat 528  
 Pro Pro Trp Arg Gln Ala Ala Pro Phe Ala Leu Ser Ala Leu Leu Tyr  
 85 90 95  
 ggc gct aac aac aac ctg gtg atc tat ctt cag cgt tac atg gac ccc 576  
 Gly Ala Asn Asn Asn Leu Val Ile Tyr Leu Gln Arg Tyr Met Asp Pro  
 100 105 110  
 agc acc tac cag gtg ctg agt aat ctc aag att gga agc aca gct gtg 624  
 Ser Thr Tyr Gln Val Leu Ser Asn Leu Lys Ile Gly Ser Thr Ala Val  
 115 120 125  
 ctc tac tgc ctc tgc ctc cgg cac cgc ctc tct gtg cgt cag ggg tta 672

Leu Tyr Cys Leu Cys Leu Arg His Arg Leu Ser Val Arg Gln Gly Leu  
 130 135 140  
 gcg ctg ctg ctg ctg atg gct gcg gga gcc tgc tat gca gca ggg ggc 720  
 Ala Leu Leu Leu Leu Met Ala Ala Gly Ala Cys Tyr Ala Ala Gly Gly  
 145 150 155 160  
 ctt caa gtt ccc ggg aac acc ctt ccc agt ccc cct cca gca gct gct 768  
 Leu Gln Val Pro Gly Asn Thr Leu Pro Ser Pro Pro Pro Ala Ala Ala  
 165 170 175  
 gcc agc ccc atg ccc ctg cat atc act ccg cta ggc ctg ctg ctc ctc 816  
 Ala Ser Pro Met Pro Leu His Ile Thr Pro Leu Gly Leu Leu Leu Leu  
 180 185 190  
 att ctg tac tgc ctc atc tca ggc ttg tgc tca gtg tac aca gag ctg 864  
 Ile Leu Tyr Cys Leu Ile Ser Gly Leu Ser Ser Val Tyr Thr Glu Leu  
 195 200 205  
 ctc atg aag cga cag cgg ctg ccc ctg gca ctt cag aac ctc ttc ctc 912  
 Leu Met Lys Arg Gln Arg Leu Pro Leu Ala Leu Gln Asn Leu Phe Leu  
 210 215 220  
 tac act ttt ggt gtg ctt ctg aat cta ggt ctg cat gct ggc ggc ggc 960  
 Tyr Thr Phe Gly Val Leu Leu Asn Leu Gly Leu His Ala Gly Gly Gly  
 225 230 235 240  
 tct ggc cca ggc ctc ctg gaa ggt ttc tca gga tgg gca gca ctc gtg 1008  
 Ser Gly Pro Gly Leu Leu Glu Gly Phe Ser Gly Trp Ala Ala Leu Val  
 245 250 255  
 gtg ctg agc cag gca cta aat gga ctg ctc atg tct gct gtc atg aag 1056  
 Val Leu Ser Gln Ala Leu Asn Gly Leu Leu Met Ser Ala Val Met Lys

260 265 270  
 cat ggc agc agc atc aca cgc ctc ttt gtg gtg tcc tgc tgc ctg gtg 1104  
 His Gly Ser Ser Ile Thr Arg Leu Phe Val Val Ser Cys Ser Leu Val  
 275 280 285  
 gtc aac gcc gtg ctc tca gca gtc ctg cta cgg ctg cag ctc aca gcc 1152  
 Val Asn Ala Val Leu Ser Ala Val Leu Leu Arg Leu Gln Leu Thr Ala  
 290 295 300  
 gcc ttc ttc ctg gcc aca ttg ctc att gcc ctg gcc atg cgc ctg tac 1200  
 Ala Phe Phe Leu Ala Thr Leu Leu Ile Gly Leu Ala Met Arg Leu Tyr  
 305 310 315 320  
 tat ggc agc cgc tagtcctga caacttccac cctgattcag gaccctgt 1250  
 Tyr Gly Ser Arg  
 agattggggc ccaccaccag atccccctcc caggecttcc tccctctccc atcagcagcc 1310  
 ctgtaacaag tgccttgta gaaaagctgg agaagtgagg gcagccaggt tattctctgg 1370  
 aggttggtgg atgaaggggt acccctagga gatgtgaagt gtgggtttgg ttaaggaaat 1430  
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<210> 28

<211> 1738

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (95)... (508)

<400> 28

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Met Gly Phe Gly Ala Thr

1

5

ttg gcc gtt ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc 160

Leu Ala Val Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile

10

15

20

atc tgc ttc acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga 208

Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg

25

30

35

cca cgt ccg gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc 256  
 Pro Arg Pro Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala  
 40 45 50  
 cct tat cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc 304  
 Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser  
 55 60 65 70  
 tac cag gcc tac cac acc atg ccg cct cag cca ggg atg cca gca gca 352  
 Tyr Gln Gly Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala  
 75 80 85  
 ccc tac cca atg cag tac cca cca cct tac cca gcc cag ccc atg gcc 400  
 Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly  
 90 95 100  
 cca ccg gcc tac cac gag acc ctg gct gga gga gca gcc gcg ccc tac 448  
 Pro Pro Ala Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr  
 105 110 115  
 ccc gcc agc cag cct cct tac aac ccg gcc tac atg gat gcc ccg aag 496  
 Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys  
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 gcg gcc ctc tgagcattcc ctggcctctc tggtgccac ttggttatgt tgtgt 550  
 Ala Ala Leu  
 135  
 gtgtgcgtga gtggtgtgca ggcgcggttc cttacgcccc atgtgtgctg tgtgtgtcca 610  
 ggcacggttc cttacgcccc atgtgtgctg tgtgtgtcct gctgtatat gtggcttcct 670  
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 ctttctgtgt gatgcagatg tgtccctggt tcggcagcgt agccagctgc tgetttaggc 970  
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<210> 29

<211> 1930

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (82)... (1017)



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ctctgcgcgt ccgacggcga c atg ggc gtc ccc acg gcc ctg gag gcc ggc 111

Met Gly Val Pro Thr Ala Leu Glu Ala Gly

1 5 10

agc tgg cgc tgg gga tcc ctg ctc ttc gct ctc ttc ctg gct ggc tcc 159

Ser Trp Arg Trp Gly Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser

15 20 25

cta ggt cgc gtg gca gcc ttc aag gtc gcc acg ccg tat tcc ctg tat 207

Leu Gly Pro Val Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr

30 35 40

gtc tgt ccc gag ggc cag aac gtc acc ctc acc tgc agg ctc ttg ggc 255

Val Cys Pro Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly

45 50 55

cct gtg gac aaa ggc cac gat gtg acc ttc tac aag acg tgg tac cgc 303

Pro Val Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg

60 65 70

agc tcg agg ggc gag gtg cag acc tgc tca gag cgc cgg ccc atc cgc 351

Ser Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg

75 80 85 90

aac ctc acg ttc cag gac ctt cac ctg cac cat gga ggc cac cag gct 399

Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln Ala

95 100 105

gcc aac acc agc cac gac ctg gct cag cgc cac ggc ctg gag tcg gcc 447

Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu Ser Ala  
110 115 120  
tcc gac cac cat gcc aac ttc tcc atc acc atg cgc aac ctg acc ctg 495  
Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn Leu Thr Leu  
125 130 135  
ctg gat agc gcc ctc tac tgc tgc ctg gtg gtg gag atc agg cac cac 543  
Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu Ile Arg His His  
140 145 150  
cac tcg gag cac agg gtc cat ggt gcc atg gaa ctg cag gtg cag aca 591  
His Ser Glu His Arg Val His Gly Ala Met Glu Leu Gln Val Gln Thr  
155 160 165 170  
gcc aaa gat gca cca tcc aac tgt gtg gtg tac cca tcc tcc tcc cag 639  
Gly Lys Asp Ala Pro Ser Asn Cys Val Val Tyr Pro Ser Ser Ser Gln  
175 180 185  
gag agt gaa aac atc acg gct gca gcc ctg gct acg ggt gcc tgc atc 687  
Glu Ser Glu Asn Ile Thr Ala Ala Ala Leu Ala Thr Gly Ala Cys Ile  
190 195 200  
gta gga atc ctc tgc ctc ccc ctc atc ctg ctc ctg gtc tac aag caa 735  
Val Gly Ile Leu Cys Leu Pro Leu Ile Leu Leu Leu Val Tyr Lys Gln  
205 210 215  
agg cag gca gcc tcc aac cgc cgt gcc cag gag ctg gtg cgg atg gac 783  
Arg Gln Ala Ala Ser Asn Arg Arg Ala Gln Glu Leu Val Arg Met Asp  
220 225 230  
agc aac att caa ggg att gaa aac ccc gcc ttt gaa gcc tca cca cct 831  
Ser Asn Ile Gln Gly Ile Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro

235	240	245	250	
gcc cag ggg ata ccc gag gcc aaa gtc agg cac ccc ctg tcc tat gtg				879
Ala Gln Gly Ile Pro Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val				
	255	260	265	
gcc cag cgg cag cct tct gag tct ggg cgg cat ctg ctt teg gag ccc				927
Ala Gln Arg Gln Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro				
	270	275	280	
age acc ccc ctg tct cct cca ggc ccc gga gac gtc ttc ttc cca tcc				975
Ser Thr Pro Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser				
	285	290	295	
ctg gac cct gtc cct gac tct cca aac ttt gag gtc atc tagccc				1020
Leu Asp Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile				
	300	305	310	
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gtgctgaggg aggtgggtgg ggccttctgg gaaggtgagt ggagaggggc acctgcccc 1800  
 cgccctcccc atccctact cccactgtc agcgcgggccc attgcaagg tgccacacaa 1860  
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<210> 30

<211> 1892

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (5)... (1636)

<400> 30

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 gag tgg ggg cag cgg cta ctt ctg gtg ctg ctg ttg ggt ggc tgc tcc 97  
 Glu Trp Gly Gln Arg Leu Leu Leu Val Leu Leu Gly Gly Cys Ser  
 20 25 30  
 ggg cgc atc cac cgg ctg gcg ctg acg ggg gag aag cga gcg gac atc 145  
 Gly Arg Ile His Arg Leu Ala Leu Thr Gly Glu Lys Arg Ala Asp Ile  
 35 40 45  
 cag ctg aac agc ttc ggt ttc tac acc aat ggc tct ctg gag gtg gag 193

Gln Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val Glu  
 50 55 60  
 ttg agc gtc ctg cgg ctg ggc ctc cgg gag gca gaa gag aag tcc ctg 241  
 Leu Ser Val Leu Arg Leu Gly Leu Arg Glu Ala Glu Glu Lys Ser Leu  
 65 70 75  
 ctg gtg ggg ttc agt ctc agc cgg gtt cgg tct ggc aga gtt cgc tcc 289  
 Leu Val Gly Phe Ser Leu Ser Arg Val Arg Ser Gly Arg Val Arg Ser  
 80 85 90 95  
 tat tca acc cgg gat ttc cag gac tgc cct ctc cag aaa aac agt agc 337  
 Tyr Ser Thr Arg Asp Phe Gln Asp Cys Pro Leu Gln Lys Asn Ser Ser  
 100 105 110  
 agt ttc ctg gtc ctg ttc ctc atc aac acc aag gat ctg cag gtc cag 385  
 Ser Phe Leu Val Leu Phe Leu Ile Asn Thr Lys Asp Leu Gln Val Gln  
 115 120 125  
 gtg cgg aag tat gga gag cag aag acg ttg ttt atc ttt ccc ggg ctc 433  
 Val Arg Lys Tyr Gly Glu Gln Lys Thr Leu Phe Ile Phe Pro Gly Leu  
 130 135 140  
 ctc ccg gaa gca ccc tcc aaa cca ggg ctc ccg aag cca cag gcc aca 481  
 Leu Pro Glu Ala Pro Ser Lys Pro Gly Leu Pro Lys Pro Gln Ala Thr  
 145 150 155  
 gtc ccc cgc aag gtg gat ggc gga ggg acc tct gca gcc agc aag ccc 529  
 Val Pro Arg Lys Val Asp Gly Gly Gly Thr Ser Ala Ala Ser Lys Pro  
 160 165 170 175  
 aag tca aca ccc gca gtg att cag ggt cct agt ggg aag gac aag gac 577  
 Lys Ser Thr Pro Ala Val Ile Gln Gly Pro Ser Gly Lys Asp Lys Asp

180 185 190  
ctg gtg ttg ggc ctg agc cac ctc aac aac tcc tac aac ttc agt ttc 625  
Leu Val Leu Gly Leu Ser His Leu Asn Asn Ser Tyr Asn Phe Ser Phe  
195 200 205  
cac gtg gtg atc ggc tct cag gcg gaa gaa ggc cag tac agc ctg aac 673  
His Val Val Ile Gly Ser Gln Ala Glu Glu Gly Gln Tyr Ser Leu Asn  
210 215 220  
ttc cac aac tgc aac aat tca gtg cca gga aag gag cat cca ttc gac 721  
Phe His Asn Cys Asn Asn Ser Val Pro Gly Lys Glu His Pro Phe Asp  
225 230 235  
atc acg gtg atg atc cgg gag aag aac ccc gat ggc ttc ctg tgc gca 769  
Ile Thr Val Met Ile Arg Glu Lys Asn Pro Asp Gly Phe Leu Ser Ala  
240 245 250 255  
gcg gag atg ccc ctt ttc aag ctc tac atg gtc atg tcc gcc tgc ttc 817  
Ala Glu Met Pro Leu Phe Lys Leu Tyr Met Val Met Ser Ala Cys Phe  
260 265 270  
ctg gcc gct ggc atc ttc tgg gtg tcc atc ctc tgc agg aac acg tac 865  
Leu Ala Ala Gly Ile Phe Trp Val Ser Ile Leu Cys Arg Asn Thr Tyr  
275 280 285  
agc gtc ttc aag atc cac tgg ctc atg gcg gcc ttg gcc ttc acc aag 913  
Ser Val Phe Lys Ile His Trp Leu Met Ala Ala Leu Ala Phe Thr Lys  
290 295 300  
agc atc tct ctc ctc ttc cac agc atc aac tac tac ttc atc aac agc 961  
Ser Ile Ser Leu Leu Phe His Ser Ile Asn Tyr Tyr Phe Ile Asn Ser  
305 310 315

cag ggc cac ccc atc gaa ggc ctt gcc gtc atg tac tac atc gca cac 1009  
 Gln Gly His Pro Ile Glu Gly Leu Ala Val Met Tyr Tyr Ile Ala His  
 320 325 330 335  
 ctg ctg aag ggc gcc ctc ctc ttc atc acc atc gcc ctg att ggc tca 1057  
 Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala Leu Ile Gly Ser  
 340 345 350  
 ggc tgg gcc ttc atc aag tac gtc ctg tgc gat aag gag aag aag gtc 1105  
 Gly Trp Ala Phe Ile Lys Tyr Val Leu Ser Asp Lys Glu Lys Lys Val  
 355 360 365  
 ttt ggg atc gtg atc ccc atg cag gtc ctg gcc aac gtg gcc tac atc 1153  
 Phe Gly Ile Val Ile Pro Met Gln Val Leu Ala Asn Val Ala Tyr Ile  
 370 375 380  
 atc atc gag tcc cgc gag gaa ggc gcc agc gac tac gtg ctg tgg aag 1201  
 Ile Ile Glu Ser Arg Glu Glu Gly Ala Ser Asp Tyr Val Leu Trp Lys  
 385 390 395  
 gag att ttg ttc ctg gtg gac ctc atc tgc tgt ggt gcc atc ctg ttc 1249  
 Glu Ile Leu Phe Leu Val Asp Leu Ile Cys Cys Gly Ala Ile Leu Phe  
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 Pro Val Val Trp Ser Ile Arg His Leu Gln Asp Ala Ser Gly Thr Asp  
 420 425 430  
 ggg aag gtg gca gtg aac ctg gcc aag ctg aag ctg ttc cgg cat tac 1345  
 Gly Lys Val Ala Val Asn Leu Ala Lys Leu Lys Leu Phe Arg His Tyr  
 435 440 445  
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Tyr Val Met Val Ile Cys Tyr Val Tyr Phe Thr Arg Ile Ile Ala Ile  
 450 455 460  
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 Leu Leu Gln Val Ala Val Pro Phe Gln Trp Gln Trp Leu Tyr Gln Leu  
 465 470 475  
 ttg gtg gag ggc tcc acc ctg gcc ttc ttc gtg etc acg ggc tac aag 1489  
 Leu Val Glu Gly Ser Thr Leu Ala Phe Phe Val Leu Thr Gly Tyr Lys  
 480 485 490 495  
 ttc cag ccc aca ggg aac aac ccg tac ctg cag ctg ccc cag gag gac 1537  
 Phe Gln Pro Thr Gly Asn Asn Pro Tyr Leu Gln Leu Pro Gln Glu Asp  
 500 505 510  
 gag gag gat gtt cag atg gag caa gta atg acg gac tct ggg ttc cgg 1585  
 Glu Glu Asp Val Gln Met Glu Gln Val Met Thr Asp Ser Gly Phe Arg  
 515 520 525  
 gaa ggc etc tcc aaa gtc aac aaa aca gcc agc ggg cgg gaa ctg tta 1633  
 Glu Gly Leu Ser Lys Val Asn Lys Thr Ala Ser Gly Arg Glu Leu Leu  
 530 535 540  
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